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#2   #2
          OIPE

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RAW SEQUENCE LISTING   DATE: 02/02/2001
PATENT APPLICATION: US/09/765,034   TIME: 11:38:03

Input Set : A:\CN01084 sequence listing.txt
Output Set: N:\CRF3\02022001\I765034.raw

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     3 <110> APPLICANT: Hedrick, Joseph A.
     4        Lachowicz, Jean E.
     5        Wang, Wei
     6        Gustafson, Eric L.
     8 <120> TITLE OF INVENTION: Adenosine Receptor
    10 <130> FILE REFERENCE: CN01084
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/765,034
C--> 13 <141> CURRENT FILING DATE: 2001-01-17
    15 <160> NUMBER OF SEQ ID NOS: 4
    17 <170> SOFTWARE: PatentIn Ver. 2.1
    19 <210> SEQ ID NO: 1
    20 <211> LENGTH: 1338
    21 <212> TYPE: DNA
    22 <213> ORGANISM: homo sapiens
    24 <220> FEATURE:
    25 <221> NAME/KEY: CDS
    26 <222> LOCATION: (1)..(1005)
    28 <400> SEQUENCE: 1
    29 atg ctg ggg atc atg gca tgg aat gca act tgc aaa aac tgg ctg gca      48
    30 Met Leu Gly Ile Met Ala Trp Asn Ala Thr Cys Lys Asn Trp Leu Ala
    31  1               5                  10                  15
    33 gca gag gct gcc ctg gaa aag tac tac ctt tcc att ttt tat ggg att      96
    34 Ala Glu Ala Ala Leu Glu Lys Tyr Tyr Leu Ser Ile Phe Tyr Gly Ile
    35              20                  25                  30
    37 gag ttc gtt gtg gga gtc ctt gga aat acc att gtt gtt tac ggc tac     144
    38 Glu Phe Val Val Gly Val Leu Gly Asn Thr Ile Val Val Tyr Gly Tyr
    39          35                  40                  45
    41 atc ttc tct ctg aag aac tgg aac agc agt aat att tat ctc ttt aac     192
    42 Ile Phe Ser Leu Lys Asn Trp Asn Ser Ser Asn Ile Tyr Leu Phe Asn
    43      50                  55                  60
    45 ctc tct gtc tct gac tta gct ttt ctg tgc acc ctc ccc atg ctg ata     240
    46 Leu Ser Val Ser Asp Leu Ala Phe Leu Cys Thr Leu Pro Met Leu Ile
    47  65                  70                  75                  80
    49 agg agt tat gcc aat gga aac tgg ata tat gga gac gtg ctc tgc ata     288
    50 Arg Ser Tyr Ala Asn Gly Asn Trp Ile Tyr Gly Asp Val Leu Cys Ile
    51                  85                  90                  95
    53 agc aac cga tat gtg ctt cat gcc aac ctc tat acc agc att ctc ttt     336
    54 Ser Asn Arg Tyr Val Leu His Ala Asn Leu Tyr Thr Ser Ile Leu Phe
    55              100                 105                 110
    57 ctc act ttt atc agc ata gat cga tac ttg ata att aag tat cct ttc     384
    58 Leu Thr Phe Ile Ser Ile Asp Arg Tyr Leu Ile Ile Lys Tyr Pro Phe
    59          115                 120                 125
    61 cga gaa cac ctt ctg caa aag aaa gag ttt gct att tta atc tcc ttg     432
    62 Arg Glu His Leu Leu Gln Lys Lys Glu Phe Ala Ile Leu Ile Ser Leu
    63      130                 135                 140
    65 gcc att tgg gtt tta gta acc tta gag tta cta ccc ata ctt ccc ctt     480
    66 Ala Ile Trp Val Leu Val Thr Leu Glu Leu Leu Pro Ile Leu Pro Leu
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 67 145                 150                 155                 160
 69 ata aat cct gtt ata act gac aat ggc acc acc tgt aat gat ttt gca   528
 70 Ile Asn Pro Val Ile Thr Asp Asn Gly Thr Thr Cys Asn Asp Phe Ala
 71                 165                 170                 175
 73 agt tct gga gac ccc aac tac aac ctc att tac agc atg tgt cta aca   576
 74 Ser Ser Gly Asp Pro Asn Tyr Asn Leu Ile Tyr Ser Met Cys Leu Thr
 75                 180                 185                 190
 77 ctg ttg ggg ttc ctt att cct ctt ttt gtg atg tgt ttc ttt tat tac   624
 78 Leu Leu Gly Phe Leu Ile Pro Leu Phe Val Met Cys Phe Phe Tyr Tyr
 79                 195                 200                 205
 81 aag att gct ctc ttc cta aag cag agg aat agg cag gtt gct act gct   672
 82 Lys Ile Ala Leu Phe Leu Lys Gln Arg Asn Arg Gln Val Ala Thr Ala
 83         210                 215                 220
 85 ctg ccc ctt gaa aag cct ctc aac ttg gtc atc atg gca gtg gta atc   720
 86 Leu Pro Leu Glu Lys Pro Leu Asn Leu Val Ile Met Ala Val Val Ile
 87 225                 230                 235                 240
 89 ttc tct gtg cct ttt aca ccc tat cac gtc atg cgg aat gtg agg atc   768
 90 Phe Ser Val Pro Phe Thr Pro Tyr His Val Met Arg Asn Val Arg Ile
 91                 245                 250                 255
 93 gct tca cgc ctg ggg agt tgg aag cag tat cag tgc act cag gtc gtc   816
 94 Ala Ser Arg Leu Gly Ser Trp Lys Gln Tyr Gln Cys Thr Gln Val Val
 95             260                 265                 270
 97 atc aac tcc ttt tac att gtg aca cgg cct ttg gcc ttt ctg aac agt   864
 98 Ile Asn Ser Phe Tyr Ile Val Thr Arg Pro Leu Ala Phe Leu Asn Ser
 99         275                 280                 285
101 gtc atc aac cct gtc ttc tat ttt ctt ttg gga gat cac ttc agg gac   912
102 Val Ile Asn Pro Val Phe Tyr Phe Leu Leu Gly Asp His Phe Arg Asp
103         290                 295                 300
105 atg ctg atg aat caa ctg aga cac aac ttc aaa tcc ctt aca tcc ttt   960
106 Met Leu Met Asn Gln Leu Arg His Asn Phe Lys Ser Leu Thr Ser Phe
107 305                 310                 315                 320
109 agc aga tgg gct cat gaa ctc cta ctt tca ttc aga gaa aag tga      1005
110 Ser Arg Trp Ala His Glu Leu Leu Leu Ser Phe Arg Glu Lys
W--> 111                 325                 330                 335
113 ggggcttgtg aaacagattg ttctacagat gaatctgtaa gccagttaca gttttgcctta 1065
115 actcatagac atcaatcaga gagtgtcaca gatttaacct tgatctaaag acaagttgta 1125
117 cccagagtat gtgaaaagaa tgggacgaca agaatgtact ggtttcttcc tctaagaatt 1185
119 gaaaggagtt gaactgcctt atgtttgggc atgtaactcc aaaatactag gtagtataag 1245
121 gctttctcaa tcagtgcaaa aatggaagat atataaagca acaagttgtc tgcatttgat 1305
123 cactggtcag attgtaaaaa aaaaaaaaaa aaa                              1338
126 <210> SEQ ID NO: 2
127 <211> LENGTH: 334
128 <212> TYPE: PRT
129 <213> ORGANISM: homo sapiens
131 <400> SEQUENCE: 2
132 Met Leu Gly Ile Met Ala Trp Asn Ala Thr Cys Lys Asn Trp Leu Ala
133   1               5                  10                  15
135 Ala Glu Ala Ala Leu Glu Lys Tyr Tyr Leu Ser Ile Phe Tyr Gly Ile
136             20                  25                  30
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138 Glu Phe Val Val Gly Val Leu Gly Asn Thr Ile Val Val Tyr Gly Tyr
139             35                  40                  45
141 Ile Phe Ser Leu Lys Asn Trp Asn Ser Ser Asn Ile Tyr Leu Phe Asn
142         50                  55                  60
144 Leu Ser Val Ser Asp Leu Ala Phe Leu Cys Thr Leu Pro Met Leu Ile
145 65                  70                  75                  80
147 Arg Ser Tyr Ala Asn Gly Asn Trp Ile Tyr Gly Asp Val Leu Cys Ile
148             85                  90                  95
150 Ser Asn Arg Tyr Val Leu His Ala Asn Leu Tyr Thr Ser Ile Leu Phe
151             100                 105                 110
153 Leu Thr Phe Ile Ser Ile Asp Arg Tyr Leu Ile Ile Lys Tyr Pro Phe
154         115                 120                 125
156 Arg Glu His Leu Leu Gln Lys Lys Glu Phe Ala Ile Leu Ile Ser Leu
157         130                 135                 140
159 Ala Ile Trp Val Leu Val Thr Leu Glu Leu Leu Pro Ile Leu Pro Leu
160 145                 150                 155                 160
162 Ile Asn Pro Val Ile Thr Asp Asn Gly Thr Thr Cys Asn Asp Phe Ala
163             165                 170                 175
165 Ser Ser Gly Asp Pro Asn Tyr Asn Leu Ile Tyr Ser Met Cys Leu Thr
166             180                 185                 190
168 Leu Leu Gly Phe Leu Ile Pro Leu Phe Val Met Cys Phe Phe Tyr Tyr
169         195                 200                 205
171 Lys Ile Ala Leu Phe Leu Lys Gln Arg Asn Arg Gln Val Ala Thr Ala
172         210                 215                 220
174 Leu Pro Leu Glu Lys Pro Leu Asn Leu Val Ile Met Ala Val Val Ile
175 225                 230                 235                 240
177 Phe Ser Val Pro Phe Thr Pro Tyr His Val Met Arg Asn Val Arg Ile
178             245                 250                 255
180 Ala Ser Arg Leu Gly Ser Trp Lys Gln Tyr Gln Cys Thr Gln Val Val
181             260                 265                 270
183 Ile Asn Ser Phe Tyr Ile Val Thr Arg Pro Leu Ala Phe Leu Asn Ser
184         275                 280                 285
186 Val Ile Asn Pro Val Phe Tyr Phe Leu Leu Gly Asp His Phe Arg Asp
187         290                 295                 300
189 Met Leu Met Asn Gln Leu Arg His Asn Phe Lys Ser Leu Thr Ser Phe
190 305                 310                 315                 320
192 Ser Arg Trp Ala His Glu Leu Leu Leu Ser Phe Arg Glu Lys
193                 325                 330
197 <210> SEQ ID NO: 3
198 <211> LENGTH: 37
199 <212> TYPE: DNA
200 <213> ORGANISM: Artificial Sequence
202 <220> FEATURE:
203 <223> OTHER INFORMATION: Description of Artificial Sequence: sense PCR
204       primer
206 <400> SEQUENCE: 3
207 cggaattcat gctggggatc atggcatgga atgcaac                          37
210 <210> SEQ ID NO: 4
211 <211> LENGTH: 38
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RAW SEQUENCE LISTING                    DATE: 02/02/2001
PATENT APPLICATION:  US/09/765,034      TIME: 11:38:04

        Input Set : A:\CN01084 sequence listing.txt
        Output Set: N:\CRF3\02022001\I765034.raw

212 <212> TYPE: DNA
213 <213> ORGANISM: Artificial Sequence
215 <220> FEATURE:
216 <223> OTHER INFORMATION: Description of Artificial Sequence: antisense PCR
217       primer
219 <400> SEQUENCE: 4
220 tatgcggccg cccaccacac tggactagtg gatcctca                        38
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VERIFICATION SUMMARY   DATE: 02/02/2001
PATENT APPLICATION: US/09/765,034   TIME: 11:38:05

        Input Set : **A:\CN01084 sequence listing.txt**
        Output Set: **N:\CRF3\02022001\I765034.raw**

L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:111 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1